



1600

RAW SEQUENCE LISTING

DATE: 02/03/2003

PATENT APPLICATION: US/08/981,087B

TIME: 11:00:05

Input Set : A:\SEQ LIST.txt

Output Set: N:\CRF4\02032003\H981087B.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Elmore, Michael J.

7 Mauchline, Margaret L.

8 Minton, Nigel P.

9 Pasechnik, Vladimir A.

10 Titball, Richard W.

12 (ii) TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF

14 (iii) NUMBER OF SEQUENCES: 8

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: NIXON & VANDERHYE P.C.

18 (B) STREET: 1100 North Glebe Rd. 8th floor

19 (C) CITY: Arlington

20 (D) STATE: VA

21 (E) COUNTRY: USA

22 (F) ZIP: 22201-4741

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/08/981,087B

C--> 32 (B) FILING DATE: 27-May-1998

33 (C) CLASSIFICATION:

39 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: PCT/GB96/01409

37 (B) FILING DATE: 12-JUN-1996

40 (A) APPLICATION NUMBER: GB 9511909.5

41 (B) FILING DATE: 12-JUN-1995

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Crawford, Arthur R.

45 (B) REGISTRATION NUMBER: 25,327

46 (C) REFERENCE/DOCKET NUMBER: 124-688

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: 703-816-4000

50 (B) TELEFAX: 703-816-4100

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 431 amino acids

57 (B) TYPE: amino acid

58 (C) STRANDEDNESS:

59 (D) TOPOLOGY: linear

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61 (ii) MOLECULE TYPE: peptide
66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68 Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu Tyr
69 1 5 10 15
71 Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn
72 20 25 30
74 Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly
75 35 40 45
77 Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser
78 50 55 60
80 Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr
81 65 70 75 80
83 Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro
84 85 90 95
86 Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile Asp
87 100 105 110
89 Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr Asn
90 115 120 125
92 Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys Leu
93 130 135 140
95 Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn Lys
96 145 150 155 160
98 Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg Ile
99 165 170 175
101 Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu Gly
102 180 185 190
104 Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys Asn
105 195 200 205
107 Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr Glu
108 210 215 220
110 Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp Pro
111 225 230 235 240
113 Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys Arg
114 245 250 255
116 Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn
117 260 265 270
119 Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro
120 275 280 285
122 Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile
123 290 295 300
125 Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val Arg
126 305 310 315 320
128 Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu Tyr
129 325 330 335
131 Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys
132 340 345 350
134 Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile Val
135 355 360 365
137 Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn

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138          370          375          380
140 Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala
141 385          390          395          400
143 Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn Gly
144          405          410          415
146 Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
147          420          425          430
149 (2) INFORMATION FOR SEQ ID NO: 2:
151 (i) SEQUENCE CHARACTERISTICS:
152 (A) LENGTH: 144 amino acids
153 (B) TYPE: amino acid
154 (C) STRANDEDNESS:
155 (D) TOPOLOGY: linear
156 (ii) MOLECULE TYPE: peptide
162 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
164 Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu Tyr
165 1 5 10 15
167 Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn
168 20 25 30
170 Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly
171 35 40 45
173 Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser
174 50 55 60
176 Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr
177 65 70 75 80
179 Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro
180 85 90 95
182 Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile Asp
183 100 105 110
185 Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr Asn
186 115 120 125
188 Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys Leu
189 130 135 140
192 (2) INFORMATION FOR SEQ ID NO: 3:
194 (i) SEQUENCE CHARACTERISTICS:
195 (A) LENGTH: 144 amino acids
196 (B) TYPE: amino acid
197 (C) STRANDEDNESS:
198 (D) TOPOLOGY: linear
199 (ii) MOLECULE TYPE: peptide
205 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
207 Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn Lys
208 1 5 10 15
210 Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg Ile
211 20 25 30
213 Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu Gly
214 35 40 45
216 Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys Asn
217 50 55 60

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219   Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr Glu
220   65                               70                               75                               80
222   Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp Pro
223                               85                               90                               95
225   Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys Arg
226                               100                              105                              110
228   Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn
229                               115                              120                              125
231   Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro
232   130                               135                               140

```

235 (2) INFORMATION FOR SEQ ID NO: 4:

237 (i) SEQUENCE CHARACTERISTICS:

238 (A) LENGTH: 143 amino acids

239 (B) TYPE: amino acid

240 (C) STRANDEDNESS:

241 (D) TOPOLOGY: linear

243 (ii) MOLECULE TYPE: peptide

248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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250   Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile
251   1           5           10           15
253   Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val Arg
254           20           25           30
256   Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu Tyr
257           35           40           45
259   Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys
260           50           55           60
262   Leu Ile Arg Thr Ser Asn Asn Ser Leu Gly Gln Ile Ile Val
263           65           70           75           80
265   Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn
266           85           90           95
268   Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala
269           100          105          110
271   Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn Gly
272           115          120          125
274   Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
275           130          135          140

```

277 (2) INFORMATION FOR SEQ ID NO: 5:

279 (i) SEQUENCE CHARACTERISTICS:

280 (A) LENGTH: 1293 base pairs

281 (B) TYPE: nucleic acid

282 (C) STRANDEDNESS: double

283 (D) TOPOLOGY: linear

285 (ii) MOLECULE TYPE: DNA (genomic)

290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

292 TCATATACTA ATGATAAAAT TCTAATTTTA TATTTTAATA AATTATATAA AAAAATTAAA      60
294 GATAACTCTA TTTTAGATAT GCGATATGAA AATAATAAAT TTATAGATAT CTCTGGATAT      120
296 GGTTCAAATA TAAGCATTAA TGGAGATGTA TATATTTATT CAACAAATAG AAATCAATTT      180
298 GGAATATATA GTAGTAAGCC TAGTGAAGTT AATATAGCTC AAAATAATGA TATTATATAC      240
300 AATGGTAGAT ATCAAAATTT TAGTATTAGT TTCTGGGTAA GGATTCCTAA ATACTTCAAT      300

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302 AAAGTGAATC TTAATAATGA ATATACTATA ATAGATTGTA TAAGGAATAA TAATTCAGGA      360
304 TGGAAAATAT CACTTAATTA TAATAAAATA ATTTGGACTT TACAAGATAC TGCTGGAAAT      420
306 AATCAAAAAC TAGTTTTTAA TTATACACAA ATGATTAGTA TATCTGATTA TATAAATAAA      480
308 TGGATTTTTG TAACTATTAC TAATAATAGA TTAGGCAATT CTAGAATTTA CATCAATGGA      540
310 AATTTAATAG ATGAAAAATC AATTTCGAAT TTAGGTGATA TTCATGTTAG TGATAATATA      600
312 TTATTTAAAA TTGTTGGTTG TAATGATACA AGATATGTTG GTATAAGATA TTTTAAAGTT      660
314 TTTGATACGG AATTAGGTAA AACAGAAATT GAGACTTTAT ATAGTGATGA GCCAGATCCA      720
316 AGTATCTTAA AAGACTTTTG GGGAAATTAT TTGTTATATA ATAAAAGATA TTATTTATTG      780
318 AATTTACTAA GAACAGATAA GTCATTACT CAGAAATCAA ACTTTCTAAA TATTAATCAA      840
320 CAAAGAGGTG TTTATCAGAA ACCAAATATT TTTTCCAACA CTAGATTATA TACAGGAGTA      900
322 GAAGTTATTA TAAGAAAAAA TGGATCTACA GATATATCTA ATACAGATAA TTTTGTTAGA      960
324 AAAAATGATC TGGCATATAT TAATGTAGTA GATCGTGATG TAGAATATCG GCTATATGCT     1020
326 GATATATCAA TTGCAAAACC AGAGAAAATA ATAAAATTAA TAAGAACATC TAATCAAAC      1080
328 AATAGCTTAG GTCAAAATAT AGTTATGGAT TCAATAGGAA ATAATTGCAC AATGAATTTT      1140
330 CAAAACAATA ATGGGGGCAA TATAGGATTA CTAGGTTTTC ATTCAAATAA TTTGGTTGCT      1200
332 AGTAGTTGGT ATTATAACAA TATACGAAAA AATACTAGCA GTAATGGATG CTTTGGAGT      1260
334 TTTATTCTTA AAGAGCATGG ATGGCAAGAA AAC                                     1293
336 (2) INFORMATION FOR SEQ ID NO: 6:
338     (i) SEQUENCE CHARACTERISTICS:
339         (A) LENGTH: 1313 base pairs
340         (B) TYPE: nucleic acid
341         (C) STRANDEDNESS: double
342         (D) TOPOLOGY: linear
344     (ii) MOLECULE TYPE: DNA (genomic)
349     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
351 GGATCCATAT GTCTTACACT AACGACAAAA TCCTGATCCT GTAAGTCAAC AAAGTGTACA      60
353 AAAAAATCAA AGACAACTCT ATCCTGGACA TGGCTTACGA AAACAACAAA TTCATCGACA      120
355 TCTCTGGCTA TGGTTCTAAC ATCTCTATCA ACGGTGACGT CTACATCTAC TCTACTAACC      180
357 GCAACCAGTT CGGTATCTAC TCTTCTAAAC CGTCTGAAGT AAACATCGCT CAGAACAACG      240
359 ACATCATCTA CAACGGTCGT TACCAGAACT TCTCTATCTC TTTCTGGGTT CGTATCCCGA      300
361 AATACTTCAA CAAAGTTAAC CTGAACAACG AATACACTAT CATCGACTGC ATCCGTAACA      360
363 ACAACTCTGG TTGGAATATC TCTCTGAAC ACAACAAAAT CATCTGGACT CTGCAGGACA      420
365 CTGCTGGTAA CAACCAGAAA CTGGTTTTC ACTACACTCA GATGATCTCT ATCTCTGACT      480
367 ACATTAATAA ATGGATCTTC GTTACTATCA CTAACAACCG TCTGGGTAACT TCTCGTATCT      540
369 ACATCAACGG TAACCTGATC GATGAAAAAT CTATCTCTAA CCTGGGTGAC ATCCACGTTT      600
371 CTGACAACAT CCTGTTCAAA ATCGTTGGTT GCAACGACAC GCGTTACGTT GGTATCCGTT      660
373 ACTTCAAAGT TTTTCGACACT GAACTGGGTA AAACAGAAAT CGAAACTCTG TACTCTGACG      720
375 AACCAGGACCC GTCTATCCTG AAAGACTTCT GGGGTAACTA CCTGCTGTAC AACAAACGTT      780
377 ACTACCTGCT GAACCTGCTC CGGACTGACA AATCTATCAC TCAGAACTCT AACTTCCTGA      840
379 ACATCAACCA GCAGCGTGGT GTTTATCAGA AACCTAATAT CTTCTCTAAC ACTCGTCTGT      900
381 AACTGTTGTG TGAAGTTATC ATCCGTAAAA ACGGTTCTAC TGACATCTCT AACTGACACA      960
383 ACTTCGTACG TAAAAACGAC CTGGCTTACA TCAACGTTGT TGACCGTGAC GTTGAATACC     1020
385 GTCTGTACGC TGACATCTCT ATCGCTAAAC CGGAAAAAAT CATCAAAGT ATCCGTAATT     1080
387 CTAATCTTAA CAACTCTCTG GGTGAGATCA TCGTTATGGA CTCGATCGGT ACAAAGTACA     1140
389 CTATGAACCT CCAGAACAAAC AACGGTGGTA ACATCGGTCT GCTGGGTTTC CACTCTAACA     1200
391 ACCTGGTTGC TTCTTCTTGG TACTACAACA ACATCCGTAA AAACACTTCT TCTAACGGTT     1260
393 GCTTCTGGTC TTTATCTCTT AAAGAACACG GTTGGCAGGA AAATAATCT AGA              1313
396 (2) INFORMATION FOR SEQ ID NO: 7:
398     (i) SEQUENCE CHARACTERISTICS:

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VERIFICATION SUMMARY

DATE: 02/03/2003

PATENT APPLICATION: US/08/981,087B

TIME: 11:00:06

Input Set : A:\SEQ LIST.txt

Output Set: N:\CRF4\02032003\H981087B.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]